File Name	Date Created	Size (bytes)
MakeHelp.bat	09/27/2000	1,594
newlibrarynamedlg.cpp	10/05/2000	1,926
newlibrarynamedlg.h	09/29/2000	883
resource.h	02/06/2001	8,530
resource.hm	02/06/2001	4,528
startdlg.cpp	10/23/2000	3,742
startdlg.h	10/23/2000	1,093
StdAfx.cpp	10/11/2000	221
StdAfx.h	10/03/2000	602
SubtractionLibraryUtility.cpp	10/11/2000	4,047
SubtractionLibraryUtility.h	02/06/2001	6,385
SubtractionLibraryUtility.hpj	02/06/2001	2,624
SubtractionLibraryUtility.rc	07/25/2001	28,316
SubtractionLibraryUtilityDlg.cpp	06/21/2001	209,771
SubtractionLibraryUtilityDlg.h	04/16/2001	6,943
SubtractionLibraryUtility.hm	08/09/2001	663
TimedMessage.cpp	10/27/2000	1,718
TimedMessage.h	10/27/2000	875
trimdialog.cpp	11/06/2000	119,594
trimdialog.h	11/06/2000	4,099
TUTORIAL PRIMERS.VEC	06/08/2001	2,039
TUTORIAL001.Seq	06/11/2001	640

--

Replace the paragraph at page 8, line 3, with the following paragraph:

--BRIEF DESCRIPTION OF THE DRAWING

Fig. 1 shows a file directory structure for one embodiment of the invention.

Fig. 2 shows a Main User Interface computer display.

Fig. 3 (SEQ ID NOS 7, 9 and 12-16) shows a Trimming Interface computer display.--

```
Query: 278   ctgggcagcatgtgcttggtttttcttgttgctcccacaaccgaagtttnggcatcangat 337
              ||||||||||||||||||||||||||||||||||||||||| |||||| | || ||||||| |||
Sbjct: 854   ctgggcagcatgtgcttggtttttcttgttgctcccataaccgatg-ttgggcatcaggat 796
Query: 338   ntggcccttgaaccttctcc-ccncctgttgtcnatgcctctgggtttccnc--atttcn 394
               |||||||||||||||||||| |  ||||||||||| ||||||||||||||| |    ||||
Sbjct: 795   ctggcccttgaaccttctccgcaccctgttgtcaatgcctctgggtttccgccagtttcg 736
Query: 395   cttaa-tttcccatatcggtctga 417
              ||||| |||| |||||||||||||
Sbjct: 735   cttaattttcacatatcggtctga 712
```

gi|6981481|ref|NM_013226.1|| Rattus norvegicus ribsml protein L32(Rpl32),
mRNA

              Length = 465
Score = 452 bits (228), Expect = e-125
 Identities = 319/350 (91%), Gaps = 2/350 (0%)
 Strand = Plus / Minus
Query: SEQ ID NO: 3

```
        38   gcaggttttgtgatttttatttaaacataaaacatgcacacaagccatctactcattttct 97
              |||| |||||||| ||||||||| |||| |||||| |||||||||||||||||| ||||| |||
Sbjct: SEQ ID NO: 4
       461   gcagtttttgtggtttttatttgaacacaaaacaggcacacaagccatctattcattctct 402
Query: 98   tcgctgcgtancctggcgttgggattggtgactctgatggccagctgtgctgctctttct 157
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 401   tcgctgcgtagcctggcgttgggattggtgactctgatggccagctgtgctgctctttct 342
Query: 158   acaatggcttttcagttcttanaggacacattgtgagcaatctcagcacagtaagatttg 217
              || ||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 341   acgatggcttttcggttcttagaggacacattgtgagcaatctcagcacagtaagatttg 282
Query: 218   ttgcacatcagcagcacctccagctccttgacattgtggaccannaacttgcggaanccg 277
              |||||||||||||||||||| ||||||||||||||||||||||||  |||| |||||| |||
Sbjct: 281   ttgcacatcagcagcacttccagctccttgacattgtggaccagaaacttccggaagccg 222
Query: 278   ctgggcagcatgtgcttggtttttcttgttgctcccacaaccgaagtttnggcatcangat 337
              || ||||||||||||||||||||||||| ||||| |||| ||| |||| ||||||||| |||
Sbjct: 221   ctaggcagcatgtgcttggtttttcttgttactcccgtaacc-aatgttgggcatcaggat 163
Query: 338   ntggcccttgaaccttctcc-ccncctgttgtcnatgcctctgggtttcc 386
              ||||||||||| |||||| | ||||||||||| |||||||||||||||||
Sbjct: 162   ctggcccttgaatcttctccgcaccctgttgtcgatgcctctgggtttcc 113
```

  Database: nt
    Posted date: Mar 30, 2000 10:02 PM
  Number of letters in database: 1,816,255,750
  Number of sequences in database: 607,850

```
Lambda      K       H
    1.37     0.711       0.00
Gapped
Lambda      K       H
    1.37     0.711  4.94e-324
```
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 420761
Number of Sequences: 607850
Number of extensions: 420761
Number of successful extensions: 34073
Number of sequences better than 10.0: 52
length of query: 561
length of database: 1,816,255,750

```
effective HSP length: 20
effective length of query: 541
effective length of database: 1,804,098,750
effective search space: 976017423750
effective search space used: 976017423750
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 10 (19.8 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)
```

--

Replace the label for Table 3. at page 20, line 8, with the following label:

--Table 3. (SEQ ID NO: 5)--

Replace the paragraph at page 24, line 7 with the following paragraph:

-- A vector file must be customized for a particular laboratory and selected prior to the trimming step. The vectors files are formatted using a six line, ASCII text format. Only the first contiguous string of letters on each line is read, so the remainder of each line can be used for annotations. Each line starts with a nucleotide sequence. An example vector file is presented below (SEQ ID NOS 6-11, respectively in order of appearance):

AGCGGCCGCCCGGGCAGGTC　　// positive insertion orientation 5' adapter sequence

ACCTCGGCCGCGACCACGCT　　// positive insertion orientation 3' adapter sequence

TTACTAGTGGATCCGAGCTCGGTACCAAGCTTC　　// forward direction confirm fragment 25 bases after 3' adapter

AGCGTGGTCGCGGCCGAGGT　　// negative insertion orientation 5' adapter sequence

ACCTGCCCGGGCGGCCGCTC　　// negative insertion orientation 3' adapter sequence

CACACTGGCGGCCGCTCGAGCATGCATCTAGAG　　// reverse direction confirm fragment 25 bases after 3' adapter. --